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- <110> Sim, Gek-Kee Yang, Shumin Sellins, Karen S.
- <120> NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
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- <150> 60/078,765
- <151> 1998-03-19
- <150> 09/062,597
- <151> 1998-04-17
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987

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		cac His				_	-		-		_			-	•	159
		tac Tyr 30		_								-				207
_	_	gca Ala	_	_		-										255
•		gtt Val	-					_	-	_	-			-	-	303
		tct Ser														351
	-	gac Asp										_	-	-	-	399
-		gac Asp 110										-				447

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gac Asp	atc Ile	aaa Lys	agg Arg	ata Ile 160	atg Met	tgt Cys	tca Ser	acc Thr	tct Ser 165	gga Gly	ggt Gly	ttt Phe	cca Pro	aag Lys 170	cct Pro	591
cac His	ctc Leu	tcc Ser	tgg Trp 175	tgg Trp	gaa Glu	aat Asn	gaa Gl _. u	gaa Glu 180	gaa Glu	ttg Leu	aat Asn	gct Ala	gcc Ala 185	aac Asn	aca Thr	639
aca Thr	gtt Val	tcc Ser 190	caa Gln	gac Asp	ccg Pro	gac Asp	act Thr 195	gag Glu	ttg Leu	tac Tyr	act Thr	att Ile 200	agt Ser	agt Ser	gaa Glu	687
Leu	gat Asp 205	ttc Phe	aat Asn	ata Ile	Thr	agc Ser 210	aac Asn	cat His	agc Ser	ttt Phe	gtg Val 215	tgt Cys	ctt Leu	gtc Val	aag Lys	735
tat Tyr 220	gga Gly	gac Asp	tta Leu	aca Thr	gta Val 225	tca Ser	cag Gln	atc Ile	Phe	aac Asn 230	tgg Trp	caa Gln	aaa Lys	Cys	aag Lys 235	783
taac	attg	tt c	tgag	gagt	t tc	tact	gtgt	aaa	atct	aaa	aaga	aaat	aa c	tcag	ccaga	843
taca	tttt	gg a	atta	tgta	t gt	taac	tttg	ata	gcat	ttc	ttgt	attt	tt a	gacc	cataa	903
atga	taat	ga a	gtga	tatt	g tg	actt	gtta	agg	tcac	tgt	acag	gtat	gg c	cata	atgtt	963
acta	attt	ta t	ttcc	ttta	a ta	aacc	ttct	aaa	actg	aga	catc	caaa	aa a	aaaa	aaaaa	1023
a ⁻	-						-									1024

<210> 12

<211> 235

<212> PRT

<213> Canis familiaris

<400> 12

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Ser Gly Ile Ile Gln Val Asn Lys Thr Val Lys Glu Val Ala Val Leu 35 40 45

Ser Cys Asp Tyr Asn Ile Ser Thr Thr Glu Leu Met Lys Val Arg Ile
50 55 60

Tyr Trp Gln Lys Asp Asp Glu Val Val Leu Ala Val Thr Ser Gly Gln
65 70 .75 80

Thr Lys Val Trp Ser Lys Tyr Glu Asn Arg Thr Phe Ala Asp Phe Thr . 85 90 95

Asn Asn Leu Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly
100 105 110

Lys Tyr Thr Cys Ile Val Gln Lys Thr Glu Lys Arg Ser Tyr Lys Val

Lys His Met Thr Ser Val Met Leu Leu Val Arg Ala Asp Phe Pro Val 130 135 140

Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asp Ile Lys Arg Ile 145 150 155 160

Met Cys Ser Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Trp 165 170 175 .

Glu Asn Glu Glu Glu Leu Asn Ala Ala Asn Thr Thr Val Ser Gln Asp 180 185 190

Pro Asp Thr Glu Leu Tyr Thr Ile Ser Ser Glu Leu Asp Phe Asn Ile
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Thr Ser Asn His Ser Phe Val Cys Leu Val Lys Tyr Gly Asp Leu Thr 210 215 220

Val Ser Gln Ile Phe Asn Trp Gln Lys Cys Lys 225 230 235

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<210> 14

<211> 705

<212> DNA

<213> Canis familiaris

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acagtgaaag aagtagcagt actgtcctgt gattacaaca tttccactac agaactgatg 180
aaagttcgaa tctattggca aaaggatgat gaagtggtgc tggctgtcac atctggacaa 240
acgaaagtgt ggtccaagta tgagaatcgc acctttgctg acttcaccaa taacctctcc 300
atcgtgatta tggctctgcg cctgtcagac aatggcaaat acacctgtat cgttcaaaaag 360
actgaaaaaa ggtcttacaa agtgaaacac atgacttcgg tgatgttatt ggtcagagct 420
gacttccctg tccctagtat aactgacctt ggaaatccat cccatgacat caaaaggata 480
atgtgttcaa cctctggagg ttttccaaag cctcacctct cctggtgga aaatgaagaa 540
gaattgaatg ctgccaacac aacagttcc caagacccgg acactgagtt gtacactatt 600
agtagtgaac tggattcaa tataacaagc aaccatagct ttgtgtgtct tgtcaagtat 660
ggagacttaa cagtatcac gatcttcaac tggcaaaaat gtaag 705

<210> 15

<211> 705

<212> DNA

<213> Canis familiaris

<400> 15
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agtgtccggg tcttgggaaa ctgttgtgtt ggcagcattc aattcttct cattttccca 180
ccaggagagg tgaggctttg gaaaacctcc agaggttgaa cacattatcc ttttgatgtc 240
atgggatgga tttccaaggt cagttatact agggacaggg aagtcagctc tgaccaataa 300
catcaccgaa gtcatgtgtt tcactttgta agacctttt tcagtcttt gaacgataca 360
ggtgtatttg ccattgtctg acaggcgcag agccataatc acgatggaga ggttattggt 420
gaagtcagca aaggtgcgat tctcatactt ggaccacact ttcgtttgtc cagatgtgac 480
agccagcacc acttcatcat ccttttgcca atagattcga acttcatca gttctgtagt 540
ggaaatgttg taatcacagg acagtactgc tacttcttc actgtttgt tcacctggat 600
gatgcctgaa cagaagtaaa agagactagc tagcaccaag agctgagaga ccttgagata 660

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	_	tg t			-	_				_		ac a Asĥ I				48
	-			-				-	_		_	aag Lys	_		-	96
			-									aca Thr				144
		_	_	-	_							gac Asp			_	192
_	-	_					_					cct Pro 75			-	240
	-	-		-		-		_		-		gac Asp				288
-	-					-		-	-	-		ttg Leu			-	336
	_											atg Met			_	384
,		_										cct Pro	-		_	432

135 140 130 gta act tot aat aga aca gaa aat tot ggc atc ata aat ttg acc tgc 480 Val Thr Ser Asn Arg Thr Glu Asn Ser Gly Ile Ile Asn Leu Thr Cys 150 145 tca tcc ata caa ggt tac cca gaa ccc aag gag atg tat ttt ttg gta 528 Ser Ser Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Leu Val 160 165 170 aaa acc gag aat tca agt act aag tat gat act gtc atg aag aaa tct 576 Lys Thr Glu Asn Ser Ser Thr Lys Tyr Asp Thr Val Met Lys Lys Ser 180 caa aat aat gtc aca gaa ctc tac aac gtt tct atc agc ttg tcc ttc 624 Gln Asn Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Ser Phe 200 195 tca gtc cct gaa gca agc aat gtg agc atc ttc tgt gtc ctg caa ctt 672 Ser Val Pro Glu Ala Ser Asn Val Ser Ile Phe Cys Val Leu Gln Leu 210 215 gag tca atg aag ctt ccc tcc cta cct tat aat ata gaa acc aac aaa 720 Glu Ser Met Lys Leu Pro Ser Leu Pro Tyr Asn Ile Glu Thr Asn Lys 230 768 gtg gag aga aaa gaa agt gag cag acc aag gaa aga gta cgg tac cat Val Glu Arg Lys Glu Ser Glu Gln Thr Lys Glu Arg Val Arg Tyr His 250 240 245 gaa acg gaa aga tot gat gaa goo cag tgt gtt aac att tog aag aca 816 Glu Thr Glu Arg Ser Asp Glu Ala Gln Cys Val Asn Ile Ser Lys Thr 260 265 255 gct tca ggc gac aac agt act aca cag ttt taattaaaga gtaaagtcca 866 Ala Ser Gly Asp Asn Ser Thr Thr Gln Phe 275 tccattgttt atatgccttc cctttcaaat tttggcttgc ctttttctcg tccattaata 926 ttattattqc cactaataat aagaggcttt ccagggctcc ctctaaatga gagagcctcc 986 ctataatgcc agttctgctc cctacaccag gagcagattt taactgcttc ttttcatctc 1046 agagcacact tgtgggccat gctcacctga ctggctcctg gctcaggaat aatgtttaag 1106 actaacacct cctgtttcag attcagcctt cttttcttaa ttttatacat tgtgttttat 1166

<210> 17

<211> 280

<212> PRT

<213> Canis familiaris

<400> 17

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Thr Leu Leu Tyr Gly Ala Ala Ser Met Lys Ser Gln Ala Tyr Phe
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Asn Lys Thr Gly Glu Leu Pro Cys His Phe Thr Asn Ser Gln Asn Ile 35 40 45

Ser Leu Asp Glu Leu Val Val Phe Trp Gln Asp Gln Asp Lys Leu Val
50 55 60

Leu Tyr Glu Leu Tyr Arg Gly Lys Glu Asn Pro Gln Asn Val His Arg
65 70 75 80

Lys Tyr Lys Gly Arg Thr Ser Phe Asp Lys Asp Asn Trp Thr Leu Arg 85 90 95

Leu His Asn Ile Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Phe Val

100 105 110

His His Lys Gly Pro Lys Gly Leu Val Pro Met His Gln Met Asn Ser 115 120 125

Asp Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Met Val Thr 130 135 140

Ser Asn Arg Thr Glu Asn Ser Gly Ile Ile Asn Leu Thr Cys Ser Ser 145 150 155 160

Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Leu Val Lys Thr 165 170 175

Glu Asn Ser Ser Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 180 185 190

Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Ser Phe Ser Val 195 200 205

Pro Glu Ala Ser Asn Val Ser Ile Phe Cys Val Leu Gln Leu Glu Ser 210 215 220

Met Lys Leu Pro Ser Leu Pro Tyr Asn Ile Glu Thr Asn Lys Val Glu 225 230 235 240

Arg Lys Glu Ser Glu Gln Thr Lys Glu Arg Val Arg Tyr His Glu Thr 245 250 255

Glu Arg Ser Asp Glu Ala Gln Cys Val Asn Ile Ser Lys Thr Ala Ser 260 265 270

Gly Asp Asn Ser Thr Thr Gln Phe 275 280

<210> 18

<211> 1795

<212> DNA

<213> Canis familiaris

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ctccagtctt gttgaaatat gcttgactct tcatggaagc agcaccatag agcaggaggg 1740
tcatcacaaa gagaatgtta ttcagttcca tagtgcatct gagatacatc ttggc 1795

<210> 19

<211> 840

<212> DNA

<213> Canis familiaris

<400> 19

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cattttacaa atteteaaaa cataageetg gatgagttgg tagtgttttg geaggaceag 180
gataagetgg ttetgtacga getatacaga ggeaaagaga acceeteaaaa tgtteatege 240
aagtataagg geegeacaag etttgacaaa gacaattgga eeetgagaet eeataatatt 300
cagateaagg acaagggett gtateaatgt ttegteate ataaagggee caaaggaete 360
gtteecatge accagatgaa ttetgaceta teagtgettg etaactteag teaacetgaa 420
ataatggtaa ettetaatag aacagaaaat tetggeatea taaatttgae etgeteatee 480
atacaaggtt acceagaace caaggagatg tatttttgg taaaaacega gaatteaagt 540
actaagtatg atactgteat gaagaaatet eaaaataatg teacagaact etacaacgtt 600
tetateaget tgteettete agteeetgaa geaageaatg tgageatett etgtgteetg 660
caacttgagt caatgaaget teeeteeeta eettataata tagaaaceaa caaagtggag 720
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<210> 20

<211> 840

<212> DNA

<213> Canis familiaris

<400> 20

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<210> 21

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 Primer

<400> 21

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18

<210> 22

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Primer <400> 22 22 gtagaaactc ctcagaacaa tg <210> 23 <211> 19 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic Primer <400> 23 gtagtatttt ggcaggacc 19 <210> 24 <211> 23 <212> DNA <213> Canis familiaris <400> 24 23 tagaygsgca ggtcaaattt atg <210> 25 <211> 2830 <212> DNA <213> Felis catus <220> <221> CDS <222> (179)..(1174) <400> 25 gttttttttt ttttgagttc tagtctcagc cctgacatta tttctttctc tacaaagagt 60 gttaggaagt tatggggagc tcacaaaggc tcctcatcgt ttattcttaa caccttgttt 120 ctgtgttcct cgggaatgtc actgagctta tacatctggt ctctgggagc tgcagtgg atg ggc att tgt gac agc act atg gga ctg agt cac act ctc ctt gtg 226 Met Gly Ile Cys Asp Ser Thr Met Gly Leu Ser His Thr Leu Leu Val 1 15

•	-		ctg Leu 20				-			-	_	_		_		274
			act Thr		-	-		_								322
	_	-	gat Asp		_	-	-			_	_	_	-	_	_	370
_	_		gag Glu													418
			aag Lys													466
-			aat Asn 100	_	_											514
			aaa Lys													562
	_		tca Ser													610
	Ser		aga Arg													658
			ggt Gly													706
			tca Ser 180	Thr		-			Thr							754
			aca Thr	-	_			Val					Pro			802

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aca ctg gag atg ctg ctc tcc cta cct ttc aat ata gat gca caa cct 89 Thr Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln Pro 225 230 235 240	8
aag gat aaa gac cct gaa caa ggc cac ttc ctc tgg att gcg gct gta 94 Lys Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val 245 250 255	6
ctt gta atg ttt gtt gtt ttt tgt ggg atg gtg tcc ttt aaa aca cta 99 Leu Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu 260 265 270	4 -
agg aaa agg aag aag cag cct ggc ccc tct cat gaa tgt gaa acc 10. Arg Lys Arg Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr 275 280 285	42
atc aaa agg gag aga aaa gag agc aaa cag acc aac gaa aga gta cca 109 Ile Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro 290 295 300	90
tac cac gta cct gag aga tct gat gaa gcc cag tgt att aac att ttg 113 Tyr His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu 305 310 315 320	
aag aca gcc tca ggc gac aaa agt act aca cat ttt taattaaaga 118 Lys Thr Ala Ser Gly Asp Lys Ser Thr Thr His Phe 325 330	34
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<210> 26

<211> 332

<212> PRT

<213> Felis catus

<400> 26

Met Gly Ile Cys Asp Ser Thr Met Gly Leu Ser His Thr Leu Leu Val

Met Ala Leu Leu Ser Gly Val Ser Ser Met Lys Ser Gln Ala Tyr Phe Asn Lys Thr Gly Glu Leu Pro Cys His Phe Thr Asn Ser Gln Asn Ile Ser Leu Asp Glu Leu Val Val Phe Trp Gln Asp Gln Asp Lys Leu Val Leu Tyr Glu Ile Phe Arg Gly Lys Glu Asn Pro Gln Asn Val His Leu Lys Tyr Lys Gly Arg Thr Ser Phe Asp Lys Asp Asn Trp Thr Leu Arg Leu His Asn Val Gln Ile Lys Asp Lys Gly Thr Tyr His Cys Phe Ile His Tyr Lys Gly Pro Lys Gly Leu Val Pro Met His Gln Met Ser Ser Asp Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Thr Val Thr Ser Asn Arg Thr Glu Asn Ser Gly Ile Ile Asn Leu Thr Cys Ser Ser Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn Thr Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser Val Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu Thr Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln Pro Lys Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val

Leu Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu 260 265 270

Arg Lys Arg Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr 275 280 285

Ile Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro 290 295 300

Tyr His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu 305 310 315 320

Lys Thr Ala Ser Gly Asp Lys Ser Thr Thr His Phe 325 330

<210> 27

<211> 2830

<212> DNA

<213> Felis catus

<400> 27

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<210> 28

<211> 996

<212> DNA

<213> Felis catus

<400> 28

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gtttctatca gcttgccttt ttcagtccct gaagcacaca atgtgagcgt cttttgtgcc 660 ctgaaactgg agacactgga gatgctgctc tccctacctt tcaatataga tgcacaacct 720 aaggataaag accctgaaca aggccacttc ctctggattg cggctgtact tgtaatgttt 780 gttgttttt gtgggatggt gtcctttaaa acactaagga aaaggaagaa gaagcagcct 840 ggccctctc atgaatgtga aaccatcaaa agggagagaa aagagagcaa acagaccaac 900 gaaagagtac cataccacgt acctgagaga tctgatgaag cccagtgtat taacattttg 960 aagacagcct caggcgacaa aagtactaca catttt 996

<210> 29

<211> 996

<212> DNA

<213> Felis catus

<400> 29

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ctcccttttg atggtttcac attcatgaga ggggccaggc tgcttcttct tccttttcct 180
tagtgtttta aaggacacca tcccacaaaa aacaacaaac attacaagta cagccgcaat 240
ccagaggaag tggccttgtt cagggtcttt atccttaggt tgtgcatcta tattgaaagg 300
tagggagagc agcatctcca gtgtctccag tttcagggca caaaagacgc tcacattgtg 360
tgcttcaggg actgaaaaag gcaagctgat agaaacgttg tacagttctg tcacattatt 420
ttgagatttc ttcatgacag tatcatactt agtagttgaa ttctcagtgt ttagctgaaa 480
atacatctcc ttaggttctg ggtaaccttg tattgagtga caggtcaaat ttatgatgcc 540
agaattttct gttctattag aagttactgt tattcaggt tgactgaagt tagcaagcac 600
tgataggtca gaactcattt ggtgcatggg aactagtcct ttgggccctt tataatgaat 660
gaaacagtga tatgtgccct tgtccttgat ctgaacattg tggagtctca gggtccagtt 720
gtccttgtca aagcttgtac ggcccttata tttgagatga acattttgag ggttctcttt 780

gcctctgaat atctcataca gaaccagctt atcctggtcc tgccaaaata ctaccagctc 840 atccaggett atgttttgag agtttgtaaa atggcatggc agttetecag tettgttgaa 900 atatgcttga ctcttcatgg aagaacacc agagagcagg agggccatca caaggagagt 960 gtgactcagt cccatagtgc tgtcacaaat gcccat 996

<210> 30 <211> 509 <212> DNA <213> Felis catus <220> <221> CDS <222> (1)..(507) <400> 30 ata caa ggt tac cca gaa cct aag gag atg tat ttt cag cta aac act Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn Thr 10 gag aat tca act act aag tat gat act gtc atg aag aaa tct caa aat 96 Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 20 25 aat gtg aca gaa ctg tac aac gtt tct atc agc ttg cct ttt tca gtc Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser Val cct gaa gca cac aat gtg agc gtc ttt tgt gcc ctg aaa ctq qaq aca 192 Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu Thr 50 55 ctg gag atg ctg ctc tcc cta cct ttc aat ata gat gca caa cct aaq Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln Pro Lys 65 70 gat aaa gac cet gaa caa ggc cac tte etc tgg att geg get gta ett Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val Leu 85 90 gta atg ttt gtt gtt ttt tgt ggg atg gtg tcc ttt aaa aca cta agg 336 Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu Arg 100 105 110 aaa agg aag aag cag cct ggc ccc tct cat gaa tgt gaa acc atc

384

Lys Arg Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr Ile 125 120 115 aaa agg gag aga aaa gag agc aaa cag acc aac gaa aga gta cca tac 432 Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro Tyr 135 130 cac qta cct gag aga tct gat gaa gcc cag tgt att aac att ttg aag His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu Lys 155 145 150 aca gcc tca ggc gac aaa agt act aca ca 509 Thr Ala Ser Gly Asp Lys Ser Thr Thr 165 <210> 31 <211> 169 <212> PRT <213> Felis catus <400> 31 Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn Thr 10 5 Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 25 20 Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser Val 40 Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu Thr 55 Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln Pro Lys 75 70 65 Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val Leu 90 85 Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu Arg 105 100 Lys Arg Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr Ile 120 Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro Tyr 130 135

His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu Lys 145 150 155 160

Thr Ala Ser Gly Asp Lys Ser Thr Thr 165

<210> 32

<211> 509

<212> DNA

<213> Felis catus

<400> 32

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cttttgatgg tttcacattc atgagagggg ccaggctgct tcttcttcct tttccttagt 180

gttttaaagg acaccatccc acaaaaaaca acaaacatta caagtacagc cgcaatccag 240

aggaagtggc cttgttcagg gtctttatcc ttaggttgtg catctatatt gaaaggtagg 300

gagagcagca tctccagtgt ctccagtttc agggcacaaa agacgctcac attgtgtgct 360

tcagggactg aaaaaggcaa gctgatagaa acgttgtaca gttctgtcac attatttga 420

gatttcttca tgacagtatc atacttagta gttgaattct cagtgtttag ctgaaaatac 480

atctccttag gttctgggta accttgtat

<210> 33

<211> 359

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(357)

<400> 33

ata caa ggt tac cca gaa cct aag gag atg tat ttt cag cta aac act 48

Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn Thr

1 5 10 15

gag aat toa act act aag tat gat act gtc atg aag aaa tot caa aat 96

Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 20 25 aat gtg aca gaa ctg tac aac gtt tct atc agc ttg cct ttt tca gtc Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser Val 35 40 cct gaa gca cac aat gtg agc gtc ttt tgt gcc ctg aaa ctg gag aca 192 Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu Thr 50 55 ctg gag atg ctg ctc tcc cta cct ttc aat ata gaa acc atc aaa agg Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Glu Thr Ile Lys Arg 65 70 75 gag aga aaa gag agc aaa cag acc aac gaa aga gta cca tac cac gta 288 Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro Tyr His Val 85 cct gag aga tct gat gaa gcc cag tgt att aac att ttg aag aca gcc 336 Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu Lys Thr Ala 105 100 359 tca ggc gac aaa agt act aca ca Ser Gly Asp Lys Ser Thr Thr <210> 34 <211> 119 <212> PRT <213> Felis catus <400> 34 Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn Thr 10 5 Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 20 . 25 Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser Val Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu Thr 55 Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Glu Thr Ile Lys Arg 65 70

Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro Tyr His Val 85 90 95

Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu Lys Thr Ala 100 105 110

Ser Gly Asp Lys Ser Thr Thr 115

<210> 35

<211> 359

<212> DNA

<213> Felis catus

<400> 35

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<210> 36

<211> 594

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(522)

<400> 36

atg ggt cac gca gca aag tgg aaa aca cca cta ctg aag cac cca tat 48
Met Gly His Ala Ala Lys Trp Lys Thr Pro Leu Lys His Pro Tyr
1 5 10 15

ccc aag ctc ttt ccg ctc ttg atg cta gct agt ctt ttt tac ttc tgt 96
Pro Lys Leu Phe Pro Leu Leu Met Leu Ala Ser Leu Phe Tyr Phe Cys
20 25 30

tca	ggt	atc	atc	cag	gtg	aac	aag	aca	gtg	gaa	gaa	gta	gca	gta	cta	144
Ser	Gly	Ile	Ile	Gln	Val	Asn	Lys	Thr	Val	Glu	Glu	Val	Ala	Val	Leu	
		35					40					45				
tcc	tgt	gat	tac	aac	att	tcc	acc	aaa	gaa	ctg	acg	gaa	att	cga	atc	192
Ser	Cys	Asp	Tyr	Asn	Ile	Ser	Thr	Lys	Glu	Leu	Thr	Glu	Ile	Arg	Ile	
•	50					55					60			_		
tat	tgg	caa	aag	gat	gat	gaa	atg	gtg	ttg	gct	gtc	atg	tct	qqc	aaa	240
			Lys													
65	•		3	•	70					75				2	80	
										_						
σta	caa	ata	tgg	ccc	aag	tac	aaσ	aac	cac	aca	ttc	act	gac	atc	acc	288
-			Trp		_		_		-				-	-		
				85	2	- 4 -			90		-			95		
gat	aac	cac	tcc	att	ata	atc	atσ	act	cta	cac	cta	tca	gac	aat	aac	336
-			Ser				_	_	_		_		-			550
· · · · ·			100					105	200				110		OI,	
			100					100								
222	tac	act	tgt	a++	att	caa	aao	att	ma a	222	מממ	tct	tac	222	ata	384
			Cys													204
цуs	тÀт	1115	Cys	116	116	GIII	120	116	GIU	Буз	СТУ	125	TAT	пуs	vaı	
		113					120					123				
	636	c+ a	act	+00	ata	2+4	++=	++~	at c	202	aac	at c	262	000	200	432
			Thr													432
цуз	130	пец	1111	Ser	Val	135	neu	рец	Vai	ALG	140	VAI	1111	FIO	ser	
	130			*		133					140					
3.03	~~~	666	aat	a aa	ca+	aca	~~~	c++	~ = =	a+c	2+4	3.00	cta	343	+00	480
																400
	GIU	FIO	Asn	ATG	150	AIG	Giu	теа	GIU	155	Mec	1111	ьeu	Arg		
145					130					133					160	
													.			500
_			ctg	_		_	-		-			_	tga			522
Arg	Pro	GIU	Leu	_	Ser	Arg	vaı	GIĀ		ьеи	тте	Asp				
				165					170							
gcc	accc	agg	catc	ccaa	tg a	tact	ttct	a aa	taaa	ctct	taa	aaaa	aaa	aaaa	aaaaa	582
aaa	aaaaaaaaaa aa 59								594							

<210> 37

<211> 173

<212> PRT .

<213> Felis catus

<400> 37

Met Gly His Ala Ala Lys Trp Lys Thr Pro Leu Leu Lys His Pro Tyr

1 5 10 15

Pro Lys Leu Phe Pro Leu Leu Met Leu Ala Ser Leu Phe Tyr Phe Cys 20 25 30

Ser Gly Ile Ile Gln Val Asn Lys Thr Val Glu Glu Val Ala Val Leu 35 40 45

Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr Glu Ile Arg Ile 50 55 60

Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys 65 70 75 80

Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr 85 90 95

Asp Asn His Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly
100 105 110

Lys Tyr Thr Cys Ile Ile Gln Lys Ile Glu Lys Gly Ser Tyr Lys Val 115 120 125

Lys His Leu Thr Ser Val Met Leu Leu Val Arg Gly Val Thr Pro Ser 130 135 140

Thr Glu Pro Asn Ala His Ala Glu Leu Glu Ile Met Thr Leu Arg Ser 145 150 155 160

Arg Pro Glu Leu Arg Ser Arg Val Gly Arg Leu Ile Asp 165 170

<210> 38

<211> 594

<212> DNA

<213> Felis catus

<400> 38

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ttetttggtg gaaatgttgt aateacagga tagtaetget acttetteea etgtettgtt 480
cacetggatg atacetgaae agaagtaaaa aagactaget ageateaaga geggaaagag 540
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<210> 39

<211> 519

<212> DNA

<213> Felis catus

<400> 39

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<210> 40

<211> 519

<212> DNA

<213> Felis catus

<400> 40

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condensed condensed dendardone denominal destablished official	
agtgaatgtg cggttcttgt acttgggcca cacttgtact ttgccagaca tgacagccaa	300
caccatttca tcatcctttt gccaatagat tcgaatttcc gtcagttctt tggtggaaat	360
gttgtaatca caggatagta ctgctacttc ttccactgtc ttgttcacct ggatgatacc	420
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<221> CDS <222> (60)(731)	
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tct agg acc tgg ccc tgc act gct ctg ttt tct ctt ctc ttt atc ccc Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro 20 25 30	155
gtc ttc tcc aaa ggg atg cat gtg gct cag cct gca gtg gtt ctg gcc Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala 35 40 45	203
agc agc cgg ggt gtt gct agc ttc gtg tgt gaa tat ggg tct tca ggc Ser Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ser Gly 50 55 60	251
aac gca gcc gag gtc cgg gtg aca gtg ctg cgg cag gct ggc agc cag Asn Ala Ala Glu Val Arg Val Thr Val Leu Arg Gln Ala Gly Ser Gln 65 70 75 80	299
atg act gaa gtc tgt gcc gcg aca tac aca gtg gag gat gag ttg gcc Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Ala	347

85 90 95 ttc ctg gat gat tct acc tgc acc ggc acc tcc agt gga aac aaa gtg 395 Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Ser Gly Asn Lys Val 100 105 aac ctc acc atc caa ggg ttg agg gcc atg gac acg ggg ctc tac atc 443 Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile 115 tgc aag gtg gag ctc atg tac cca ccc tac tat gta ggc atg gga 491 Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly 130 135 140 aat gga acc cag att tat gtc atc gat cct gaa cct tgc cca gat tct 539 Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser 145 15Ò 155 160 gac ttc ctc ctc tgg atc ctt gca gca gtc agt tcg ggc ttg ttt ttt 587 Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe 165 170 tat ago ttt ctt'atc aca gct gtt tct ttg ago aaa atg cta aag aaa 635 Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys 180 185 aga agc cct ctt acc aca ggg gtc tat gtg aaa atg ccc cca act gag 683 Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu 195 . 200 205 cca gaa tgt gaa aag caa ttt cag cct tat ttt att ccc atc aat tga 731 Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn 210 215 gagatcatta tgaagaagaa agaatatttt ccaatttcca ggagctgagg caattctaac 791 tttgtgctat ccagctatgt gtacttgttt gtatattttg gggggggttt catctctctt 851 taatataaag ctggatgcag aacccaaatg aagtgtacta caaattcaaa gcaaaggtgc 911 aagaaaacag agccaggatg tttctgtcac atcagatcca attttcgtaa aagtatcact 971 tgggagcaat atggggatgc agcattagga catgcgctct aggatatagg ttagggagtg 1031 gtgcggtcca aagaaagcaa aggagagaga gtcagggaga ggatgatatt gtacacactt 1091 tgtatttaca tgtgagaagt ttatagctga agtgacgttt tcaagttaaa tttttgtgct 1151

<210> 42

<211> 223

<212> PRT

<213> Canis familiaris

<400> 42

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Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro 20 25 30

Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Leu Ala 35 40 45

Ser Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ser Gly
50 55 60

Asn Ala Ala Glu Val Arg Val Thr Val Leu Arg Gln Ala Gly Ser Gln 65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Ala 85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Ser Gly Asn Lys Val

Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile 115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly 130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser 145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe 165 170 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys 180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu 195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn 210 215 220

<210> 43

<211> 1856

<212> DNA

<213> Canis familiaris

<400> 43

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<210> 44

<211> 669

<212> DNA

<213> Canis familiaris

<400> 44

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<210> 45

<211> 669

<212> DNA

<213> Canis familiaris

<400> 45

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agctgtgata agaaagctat aaaaaaacaa gcccgaactg actgctgcaa ggatccagag 180

gaggaagtca gaatctgggc aaggttcagg atcgatgaca taaatctggg ttccatttcc 240

catgcctaca tagtagggtg gtgggtacat gagctccacc ttgcagatgt agagccccgt 300

gtccatggcc ctcaaccctt ggatggtgag gttcactttg tttccactgg aggtgccggt 360

<210> 46 <211> 1883

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (69)..(740)

<400> 46

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ataaagcc atg gct tgc ttt gga ttc cgg agg cat ggg gct cag ctg gac 110

Met Ala Cys Phe Gly Phe Arg Arg His Gly Ala Gln Leu Asp

1 5 10

ctg gct tct agg acc tgg ccc tgc act gct ctg ttt tct ctt ctc ttt 158

Leu Ala Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe

15 20 25 30

atc ccc gtc ttc tcc aaa ggg atg cat gtg gcc cag cct gca gtg gtg 206 Ile Pro Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val 35 40 45

ctg gcc agc cga ggt gtc gcc agc ttc gtg tgt gaa tat ggg tct 254 Leu Ala Ser Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser 50 55 60

tca ggc aat gcc gcc gaa gtc cga gtg act gtg ctg agg cag act ggc 302 Ser Gly Asn Ala Ala Glu Val Arg Val Thr Val Leu Arg Gln Thr Gly 65 70 75

age cag atg act gaa gtc tgt gct gcg aca tac aca gtg gag aat gag 350 Ser Gln Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asn Glu 80 85 90

-	-			-	-			tgc Cys					-			398
								ttg Leu								446
								tac Tyr 135								494 ·
-					-			gtc Val		_		-		-		542
_		-						ctc Leu	-	-	-	-			-	590
			_					gct Ala								638
								GJ À āāā								686
			_					ttt Phe 215								734
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<210> 47

<211> 223

<212> PRT

<213> Felis catus

<400> 47

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Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro 20 25 30

Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala . 35 40 45

Ser Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ser Gly 50 55 60

Asn Ala Ala Glu Val Arg Val Thr Val Leu Arg Gln Thr Gly Ser Gln 65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asn Glu Leu Ala 85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Ile Ser Ser Gly Asn Lys Val 100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile 115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Ala Gly Met Gly 130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser 145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe 165 170 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys 180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn 210 215 220

<210> 48

<211> 1883

<212> DNA

<213> Felis catus

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1883

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<212> DNA

<213> Felis catus

<400> 49

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<210> 50

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<212> DNA

<213> Felis catus

<400> 50

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<213> Artificial Sequence

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<210> 57

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<220>

PCT/US99/06187

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<220>			
<223>	Description of Artificial Sequence:	Synthetic	
	Primer		
<400>	65		
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